ccggagagcc ccggagtgag cggagtagcg agtcggcaac ccggaggggt agaaatattt 60

```
ctgtc atg gct cat tca aag act agg acc aat gat gga aaa att aca tat   110
      Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr
      1               5                   10                  15

ccg cct ggg gtc aag gaa ata tca gat aaa ata tct aaa gag gag atg     158
Pro Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met
                20                  25                  30

gtg aga cga tta aag atg gtt gtg aaa act ttt atg gat atg gac cag     206
Val Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln
            35              40                  45

gac tct gaa gaa gaa aag gag ctt tat tta aac cta gct tta cat ctt     254
Asp Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu
        50                  55                  60

gct tca gat ttt ttt ctc aag cat cct ggt aaa gat gtt cgc tta ctg     302
Ala Ser Asp Phe Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu
        65                  70                  75

gta gcc tgc tgc ctt gct gat att ttc agg att tat gct cct gaa gct     350
Val Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala
80              85                  90                  95

cct tac aca tcc cct gat aaa cta aag gat ata ttt atg ttt ata aca     398
Pro Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr
                100                 105                 110

aga cag ttg aag ggg cta gag gat aca aag agc cca caa ttc aat agg     446
Arg Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg
            115                 120                 125

tat ttt tat tta ctt gag aac att gct tgg gtc aag tca tat aac ata     494
Tyr Phe Tyr Leu Leu Glu Asn Ile Ala Trp Val Lys Ser Tyr Asn Ile
            130                 135                 140

tgc ttt gag tta gaa gat agc aat gaa att ttc acc cag cta tac aga     542
Cys Phe Glu Leu Glu Asp Ser Asn Glu Ile Phe Thr Gln Leu Tyr Arg
            145                 150                 155
```

FIG. 1-1

```
acc tta ttt tca gtt ata aac aat ggc cac aat cag aaa gtc cat atg    590
Thr Leu Phe Ser Val Ile Asn Asn Gly His Asn Gln Lys Val His Met
160                 165             170             175

cac atg gta gac ctt atg agc tct att att tgt gaa ggt gat aca gtg    638
His Met Val Asp Leu Met Ser Ser Ile Ile Cys Glu Gly Asp Thr Val
            180             185             190

tct cag gag ctt ttg gat acg gtt tta gta aat ctg gta cct gct cat    686
Ser Gln Glu Leu Leu Asp Thr Val Leu Val Asn Leu Val Pro Ala His
            195             200             205

aag aat tta aac aag caa gca tat gat ttg gca aag gct tta ctg aag    734
Lys Asn Leu Asn Lys Gln Ala Tyr Asp Leu Ala Lys Ala Leu Leu Lys
            210             215             220

agg aca gct caa gct att gag cca tat att acc act ttt ttt aat cag    782
Arg Thr Ala Gln Ala Ile Glu Pro Tyr Ile Thr Thr Phe Phe Asn Gln
    225             230             235

gtt ctg atg ctt ggg aaa aca tct atc agc gat ttg tca gag cat gtc    830
Val Leu Met Leu Gly Lys Thr Ser Ile Ser Asp Leu Ser Glu His Val
240             245             250             255

ttt gac tta att ttg gag ctc tac aat att gat agt cat ttg ctg ctc    878
Phe Asp Leu Ile Leu Glu Leu Tyr Asn Ile Asp Ser His Leu Leu Leu
                260             265             270

tct gtt tta ccc cag ctt gaa ttt aaa tta aag agc aat gat aat gag    926
Ser Val Leu Pro Gln Leu Glu Phe Lys Leu Lys Ser Asn Asp Asn Glu
            275             280             285

gag cgc cta caa gtt gtt aaa cta ctg gca aaa atg ttt ggg gca aag    974
Glu Arg Leu Gln Val Val Lys Leu Leu Ala Lys Met Phe Gly Ala Lys
            290             295             300

gat tca gaa ttg gct tct caa aac aag cca ctt tgg cag tgc tac ttg    1022
Asp Ser Glu Leu Ala Ser Gln Asn Lys Pro Leu Trp Gln Cys Tyr Leu
    305             310             315

ggc agg ttt aat gat atc cat gta cca atc cgc ctg gaa tgt gtg aaa    1070
Gly Arg Phe Asn Asp Ile His Val Pro Ile Arg Leu Glu Cys Val Lys
320             325             330             335
```

FIG. 1-2

```
ttt gct agc cat tgt ctc atg aac cat cct gat tta gca aaa gac tta      1118
Phe Ala Ser His Cys Leu Met Asn His Pro Asp Leu Ala Lys Asp Leu
                340                 345                 350

aca gag tat ctt aaa gtg agg tca cat gac cct gag gaa gct att aga      1166
Thr Glu Tyr Leu Lys Val Arg Ser His Asp Pro Glu Glu Ala Ile Arg
                355                 360                 365

cat gat gtt att gtg tca ata gtt aca gct gct aaa aag gat att ctt      1214
His Asp Val Ile Val Ser Ile Val Thr Ala Ala Lys Lys Asp Ile Leu
                370                 375                 380

ctg gtc aat gat cac tta ctt aat ttt gtg aga gag aga aca tta gac      1262
Leu Val Asn Asp His Leu Leu Asn Phe Val Arg Glu Arg Thr Leu Asp
            385                 390                 395

aaa cga tgg aga gta cgc aaa gaa gcc atg atg gga ctt gcc caa att      1310
Lys Arg Trp Arg Val Arg Lys Glu Ala Met Met Gly Leu Ala Gln Ile
400                 405                 410                 415

tat aag aaa tat gct tta cag tca gca gct gga aaa gat gct gca aaa      1358
Tyr Lys Lys Tyr Ala Leu Gln Ser Ala Ala Gly Lys Asp Ala Ala Lys
                420                 425                 430

cag ata gca tgg atc aaa gac aaa ttg cta cat ata tat tat caa aat      1406
Gln Ile Ala Trp Ile Lys Asp Lys Leu Leu His Ile Tyr Tyr Gln Asn
                435                 440                 445

agt att gat gat cga cta ctt gtt gaa cgg atc ttt gct caa tac atg      1454
Ser Ile Asp Asp Arg Leu Leu Val Glu Arg Ile Phe Ala Gln Tyr Met
            450                 455                 460

gtt cct cac aat tta gaa act aca gaa cgg atg aaa tgc tta tat tac      1502
Val Pro His Asn Leu Glu Thr Thr Glu Arg Met Lys Cys Leu Tyr Tyr
465                 470                 475

ttg tat gcc aca ctg gat tta aat gct gtg aaa gca ttg aat gaa atg      1550
Leu Tyr Ala Thr Leu Asp Leu Asn Ala Val Lys Ala Leu Asn Glu Met
480                 485                 490                 495

tgg aaa tgt caa aat ctg ctc cga cat caa gta aag gat ttg ctt gac      1598
Trp Lys Cys Gln Asn Leu Leu Arg His Gln Val Lys Asp Leu Leu Asp
                500                 505                 510
```

FIG. 1-3

```
ttg att aag caa ccc aaa aca gat gcc agt gtc aag gcc ata ttt tca    1646
Leu Ile Lys Gln Pro Lys Thr Asp Ala Ser Val Lys Ala Ile Phe Ser
            515                 520                 525

aaa gtg atg gtt att aca aga aat tta cct gat cct ggt aag gct cag    1694
Lys Val Met Val Ile Thr Arg Asn Leu Pro Asp Pro Gly Lys Ala Gln
            530                 535                 540

gat ttc atg aag aaa ttc aca cag gtg tta gaa gat gat gag aaa ata    1742
Asp Phe Met Lys Lys Phe Thr Gln Val Leu Glu Asp Asp Glu Lys Ile
            545                 550                 555

aga aag cag tta gaa gta ctt gtt agt cca aca tgc tcc tgc aag cag    1790
Arg Lys Gln Leu Glu Val Leu Val Ser Pro Thr Cys Ser Cys Lys Gln
560                 565                 570                 575

gct gaa ggt tgt gtg cgt gaa ata act aag aag ttg ggc aac ccc aaa    1838
Ala Glu Gly Cys Val Arg Glu Ile Thr Lys Lys Leu Gly Asn Pro Lys
                580                 585                 590

cag cct aca aat cct ttc ctg gaa atg atc aag ttt ctc ttg gag agg    1886
Gln Pro Thr Asn Pro Phe Leu Glu Met Ile Lys Phe Leu Leu Glu Arg
                595                 600                 605

ata gca cct gtg cac ata gat acc gaa tct atc agt gct ctt att aaa    1934
Ile Ala Pro Val His Ile Asp Thr Glu Ser Ile Ser Ala Leu Ile Lys
                610                 615                 620

caa gtg aac aaa tca ata gat gga aca gca gat gat gaa gat gag ggt    1982
Gln Val Asn Lys Ser Ile Asp Gly Thr Ala Asp Asp Glu Asp Glu Gly
625                 630                 635

gtt cca act gat caa gcc atc aga gca ggt ctt gaa ctg ctt aag gta    2030
Val Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val
640                 645                 650                 655

ctc tca ttt aca cat ccc atc tca ttt cat tct gct gaa aca ttt gaa    2078
Leu Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu
                660                 665                 670

tca tta ctg gct tgt ctg aaa atg gat gat gaa aaa gta gca gaa gct    2126
Ser Leu Leu Ala Cys Leu Lys Met Asp Asp Glu Lys Val Ala Glu Ala
                675                 680                 685
```

FIG. 1-4

```
gca cta caa att ttc aaa aac aca gga agc aaa att gaa gag gat ttt    2174
Ala Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe
        690                 695                 700

cca cac atc aga tca gcc ttg ctt cct gtt tta cat cac aaa tct aaa    2222
Pro His Ile Arg Ser Ala Leu Leu Pro Val Leu His His Lys Ser Lys
    705                 710                 715

aaa gga ccc ccc cgt caa gcc aaa tat gcc att cat tgt atc cat gcg    2270
Lys Gly Pro Pro Arg Gln Ala Lys Tyr Ala Ile His Cys Ile His Ala
720                 725                 730                 735

ata ttt tct agt aaa gag acc cag ttt gca cag ata ttt gag cct ctg    2318
Ile Phe Ser Ser Lys Glu Thr Gln Phe Ala Gln Ile Phe Glu Pro Leu
                740                 745                 750

cat aag agc cta gat cca agc aac ctg gaa cat ctc ata aca cca ttg    2366
His Lys Ser Leu Asp Pro Ser Asn Leu Glu His Leu Ile Thr Pro Leu
                755                 760                 765

gtt act att ggt cat att gct ctc ctt gca cct gat caa ttt gct gct    2414
Val Thr Ile Gly His Ile Ala Leu Leu Ala Pro Asp Gln Phe Ala Ala
            770                 775                 780

cct tgg aaa tct tgg gta gct act ttc att gtg aaa gat ctt ctc atg    2462
Pro Trp Lys Ser Trp Val Ala Thr Phe Ile Val Lys Asp Leu Leu Met
    785                 790                 795

aat gat cgg ctt cca ggg aaa aag aca act aaa ctt tgg gtt cca gat    2510
Asn Asp Arg Leu Pro Gly Lys Lys Thr Thr Lys Leu Trp Val Pro Asp
800                 805                 810                 815

gaa gaa gta tct cct gag aca atg gtc aaa att cag gct att aaa atg    2558
Glu Glu Val Ser Pro Glu Thr Met Val Lys Ile Gln Ala Ile Lys Met
                820                 825                 830

atg gtt cga tgg cta ctt gga atg aaa aat aat cac agt aaa tca gga    2606
Met Val Arg Trp Leu Leu Gly Met Lys Asn Asn His Ser Lys Ser Gly
            835                 840                 845

act tct acc tta aga ttg cta aca aca ata ttg cat agt gat gga gac    2654
Thr Ser Thr Leu Arg Leu Leu Thr Thr Ile Leu His Ser Asp Gly Asp
        850                 855                 860
```

FIG. 1-5

```
ttg aca gaa cag ggg aaa att agt aaa cca gat atg tca cgt ctg aga    2702
Leu Thr Glu Gln Gly Lys Ile Ser Lys Pro Asp Met Ser Arg Leu Arg
    865                 870             875

ctt gct gct ggg agt gct att gtg aag ctg gca caa gaa ccc tgt tac    2750
Leu Ala Ala Gly Ser Ala Ile Val Lys Leu Ala Gln Glu Pro Cys Tyr
880             885             890             895

cat gaa atc atc aca tta gaa caa tat cag cta tgt gca tta gct atc    2798
His Glu Ile Ile Thr Leu Glu Gln Tyr Gln Leu Cys Ala Leu Ala Ile
                900             905                 910

aac gat gaa tgc tat caa gta aga caa gtg ttt gcc cag aaa ctt cac    2846
Asn Asp Glu Cys Tyr Gln Val Arg Gln Val Phe Ala Gln Lys Leu His
            915             920             925

aaa ggc ctt tcc cgt tta cgg ctt cca ctt gag tat atg gca atc tgt    2894
Lys Gly Leu Ser Arg Leu Arg Leu Pro Leu Glu Tyr Met Ala Ile Cys
        930             935             940

gcc ctt tgt gca aaa gat cct gta aag gag aga aga gct cat gct agg    2942
Ala Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg
    945             950             955

caa tgt ttg gtg aaa aat ata aat gta agg cgg gag tat ctg aag cag    2990
Gln Cys Leu Val Lys Asn Ile Asn Val Arg Arg Glu Tyr Leu Lys Gln
960             965             970             975

cat gca gct gtt agt gaa aaa tta ttg tct ctt cta cca gag tat gtt    3038
His Ala Ala Val Ser Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val
            980             985             990

gtt cca tat aca att cac ctt ttg gca cat gac cca gat tat gtc aaa    3086
Val Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys
        995             1000            1005

gta cag gat att gaa caa ctt aaa gat gtt aaa gaa tgt ctt tgg ttt    3134
Val Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe
    1010            1015            1020

gtt ctg gaa ata tta atg gct aaa aat gaa aat aac agt cac gct ttt    3182
Val Leu Glu Ile Leu Met Ala Lys Asn Glu Asn Asn Ser His Ala Phe
    1025            1030            1035
```

FIG. 1-6

```
atc aga aag atg gta gaa aat att aaa caa aca aaa gat gcc caa gga      3230
Ile Arg Lys Met Val Glu Asn Ile Lys Gln Thr Lys Asp Ala Gln Gly
1040            1045            1050            1055

cca gat gat gca aaa atg aat gaa aaa ctg tac act gtg tgt gat gtt      3278
Pro Asp Asp Ala Lys Met Asn Glu Lys Leu Tyr Thr Val Cys Asp Val
          1060            1065            1070

gcc atg aat atc atc atg tca aag agt act aca tac agt ttg gaa tct      3326
Ala Met Asn Ile Ile Met Ser Lys Ser Thr Thr Tyr Ser Leu Glu Ser
        1075            1080            1085

cct aaa gac ccg gta cta cca gct cgt ttc ttc act caa cct gac aag      3374
Pro Lys Asp Pro Val Leu Pro Ala Arg Phe Phe Thr Gln Pro Asp Lys
        1090            1095            1100

aat ttc agt aac acc aaa aat tat ctg cct cct gaa atg aaa tca ttt      3422
Asn Phe Ser Asn Thr Lys Asn Tyr Leu Pro Pro Glu Met Lys Ser Phe
    1105            1110            1115

ttc act cct gga aaa cct aaa aca acc aat gtt cta gga gct gtt aac      3470
Phe Thr Pro Gly Lys Pro Lys Thr Thr Asn Val Leu Gly Ala Val Asn
1120            1125            1130            1135

aag cca ctt tca tca gca ggc aag caa tct cag acc aaa tca tca cga      3518
Lys Pro Leu Ser Ser Ala Gly Lys Gln Ser Gln Thr Lys Ser Ser Arg
            1140            1145            1150

atg gaa act gta agc aat gca agc agc agc tca aat cca agc tct cct      3566
Met Glu Thr Val Ser Asn Ala Ser Ser Ser Ser Asn Pro Ser Ser Pro
        1155            1160            1165

gga aga ata aag ggg agg ctt gat agt tct gaa atg gat cac agt gaa      3614
Gly Arg Ile Lys Gly Arg Leu Asp Ser Ser Glu Met Asp His Ser Glu
        1170            1175            1180

aat gaa gat tac aca atg tct tca cct ttg ccg ggg aaa aaa agt gac      3662
Asn Glu Asp Tyr Thr Met Ser Ser Pro Leu Pro Gly Lys Lys Ser Asp
    1185            1190            1195

aag aga gac gac tct gat ctt gta agg tct gaa ttg gag aag cct aga      3710
Lys Arg Asp Asp Ser Asp Leu Val Arg Ser Glu Leu Glu Lys Pro Arg
1200            1205            1210            1215
```

FIG. 1-7

```
ggc agg aaa aaa acg ccc gtc aca gaa cag gag gag aaa tta ggt atg     3758
Gly Arg Lys Lys Thr Pro Val Thr Glu Gln Glu Glu Lys Leu Gly Met
          1220              1225              1230


gat gac ttg act aag ttg gta cag gaa cag aaa cct aaa ggc agt cag     3806
Asp Asp Leu Thr Lys Leu Val Gln Glu Gln Lys Pro Lys Gly Ser Gln
          1235              1240              1245


cga agt cgg aaa aga ggc cat acg gct tca gaa tct gat gaa cag cag     3854
Arg Ser Arg Lys Arg Gly His Thr Ala Ser Glu Ser Asp Glu Gln Gln
          1250              1255              1260


tgg cct gag gaa aag agg ctc aaa gaa gat ata tta gaa aat gaa gat     3902
Trp Pro Glu Glu Lys Arg Leu Lys Glu Asp Ile Leu Glu Asn Glu Asp
          1265              1270              1275


gaa cag aat agt ccg cca aaa aag ggt aaa aga ggc cga cca cca aaa     3950
Glu Gln Asn Ser Pro Pro Lys Lys Gly Lys Arg Gly Arg Pro Pro Lys
1280              1285              1290              1295


cct ctt ggt gga ggt aca cca aaa gaa gag cca aca atg aaa act tct     3998
Pro Leu Gly Gly Gly Thr Pro Lys Glu Glu Pro Thr Met Lys Thr Ser
               1300              1305              1310


aaa aaa gga agc aaa aaa aaa tct gga cct cca gca cca gag gag gag     4046
Lys Lys Gly Ser Lys Lys Lys Ser Gly Pro Pro Ala Pro Glu Glu Glu
          1315              1320              1325


gaa gaa gaa gaa aga caa agt gga aat acg gaa cag aag tcc aaa agc     4094
Glu Glu Glu Glu Arg Gln Ser Gly Asn Thr Glu Gln Lys Ser Lys Ser
          1330              1335              1340


aaa cag cac cga gtg tca agg aga gca cag cag aga gca gaa tct cct     4142
Lys Gln His Arg Val Ser Arg Arg Ala Gln Gln Arg Ala Glu Ser Pro
     1345              1350              1355


gaa tct agt gca att gaa tcc aca cag tcc aca cca cag aaa gga cga     4190
Glu Ser Ser Ala Ile Glu Ser Thr Gln Ser Thr Pro Gln Lys Gly Arg
1360              1365              1370              1375


gga aga cca tca aaa acg cca tca cca tca caa cca aaa aaa aat gtg     4238
Gly Arg Pro Ser Lys Thr Pro Ser Pro Ser Gln Pro Lys Lys Asn Val
          1380              1385              1390
```

FIG. 1-8

taagttgtaa atattacatt tcaaaccaat ttcaaattat tttgcaaaag ttcctaaatt 4298
End

tgtaaacata catattgctg tatttaaatt ccatatattt agccccatta cactaggtac 4358

ggcggcgaag tgctaaaagg gaacggcgat gaacaaatgt aattaataac tttctctgtg 4418

aaagctttgg aaaaatcttt tttttttttt ttttttttttg gtcaagcttg aggctgaata 4478

aagcctttga tgcacaaaat gggactgctg aagagtggac agttggacct tactttggtg 4538

accccataca tttgtggtca catgctttag ccatacacat ggtaacattg actatggagt 4598

cttgtgaaag tgtaatgtgc gatggctatg tagacataaa gaagaaactt gtaaatatct 4658

tttttctttt ttttaatgtt tctgatttct gaagtgcttg tatagctttt atctgcggct 4718

ttaaactgac agtacccgac tgtttattgg atctattgat ttgaaaagaa tttgttagga 4778

tagatcttaa gcagtaatct gtcagtgttt gtatttgtat tttctgcaat tttactgtga 4838

aaaaaaattt gttttcaaca attggtgtca ttttcttgat gtcactattt gttggagagt 4898

taaatggtct cttccctttg tgtatcttac ctagtgttta ctcctgggca cccttaatct 4958

tcagaggtgc taaattgtct gccattacac cagaaggatg cctctgatag gaggacaacc 5018

atgcaaattg tgaaatagtc ctgaagttct tggattactt tacacctcag tattgatttg 5078

tcccagaatt ttctggcctt tcatggcaat gaaaatttta agaagaaaga tttaaagtat 5138

tttaattttta aagagtgtgt tataaaataa tgtactgaat tctttatccc attttatcat 5198

cctttcagtt tttattaatc tactgtatca ataaaattct gtaatttgaa tgagtaaaaa 5258

aaaaaaaaaa aaa 5271

FIG. 1-9

55   117
LYLNLALHLLASDFFLKHPGKDVRLLVACCLADIFRIYAPEAPYTSPDKLKDIFMFITRQLKGL

196   217   241   277
LDTVLVNLVPAHKNLNKQAYDL   LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQL

319   355   375   404
LGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYL   VTAAKKDILLVNDHLLNFVRERTLDKRWRV

FIG. 2

Subdomain I, Subdomain II, Subdomain III

	β-strand		β-strand 2	β-strand 3	α-helix C
Hank's conserved regions:	β-strand		β-strand 2	β-strand 3	α-helix C
Consensus:		Mg-ATP binding loop (GxGxxGxV)		(xxxKxxx)	(xxxxExxx)
AS3 position:	419	426	453	472	489
AS3 sequence:	YALQ.SA	GKDAAKQI	LLVERIF	ERM **K** CLYYLYA	VKALN **E** MWKC
Similar protein kinase sequences:	YTLGVSA (Elm1)	GEDrfGkv (Ror2)	LLYELMD (Ykl516)	YAM **K** CLKKDVI (CeTPAI)	QAFKN **K** MQVL (Araf)
	YALINLL (Tsl)	GSGsfGdI (CK1a)	YLGEQVS (PKN2)	YAM **K** CLDKKRI (bARK1)	TLALN **E** RIML (bARK1)
	YHLKQNI (Cdc15)	AeGesHis (Ypka)	YLCLCLN (BCK1)	YAM **K** CLDKKRI (DmGPRK1)	YTRVR **E** IKFI (SME1)
	YKLVRKI (CK1a	HeSdfSev (Mik1)		VAI **K** CIAKKAL (CamKI)	
	IVLQESI (Alk5)				

Subdomain IV, Subdomain V, Subdomain VIa

	β-strand 4	β-strand 5	α-helix D	α-helix E
Hank's conserved regions:	β-strand 4	β-strand 5	α-helix D	α-helix E
Consensus:	LLDIVKDP	IFSCLVME	GNLQNFLKL	
AS3 position:	509	525	540	554
AS3 sequence:	LLDIVKDP	IFSK.VMV	GRAQDFMKK	EDDERIRKQ.LEVL
Similar protein kinase sequences:	LLDIVKDP (TPCKII)	IFSCLVME (PvpK1)	GNLQNFLKL (Let23)	ERDADAVRQILEA (CaMKIV)
	LLDWFERP (Piml)	KFSCLVME (G11a)	GSLQNFLRE (TORSO)	ECDANIMKQILSG (PICPK)
	LIGLCREA (Klg)	KFSCLVME (ZnPPK)	GNLQEYLTR (TGFbRII)	ADQLNIAKQISAG (TORRTK)
	LVKLIGYC (APK1)			ESVIMYTKQLIL (NPKI)

FIG. 3

FIG. 4
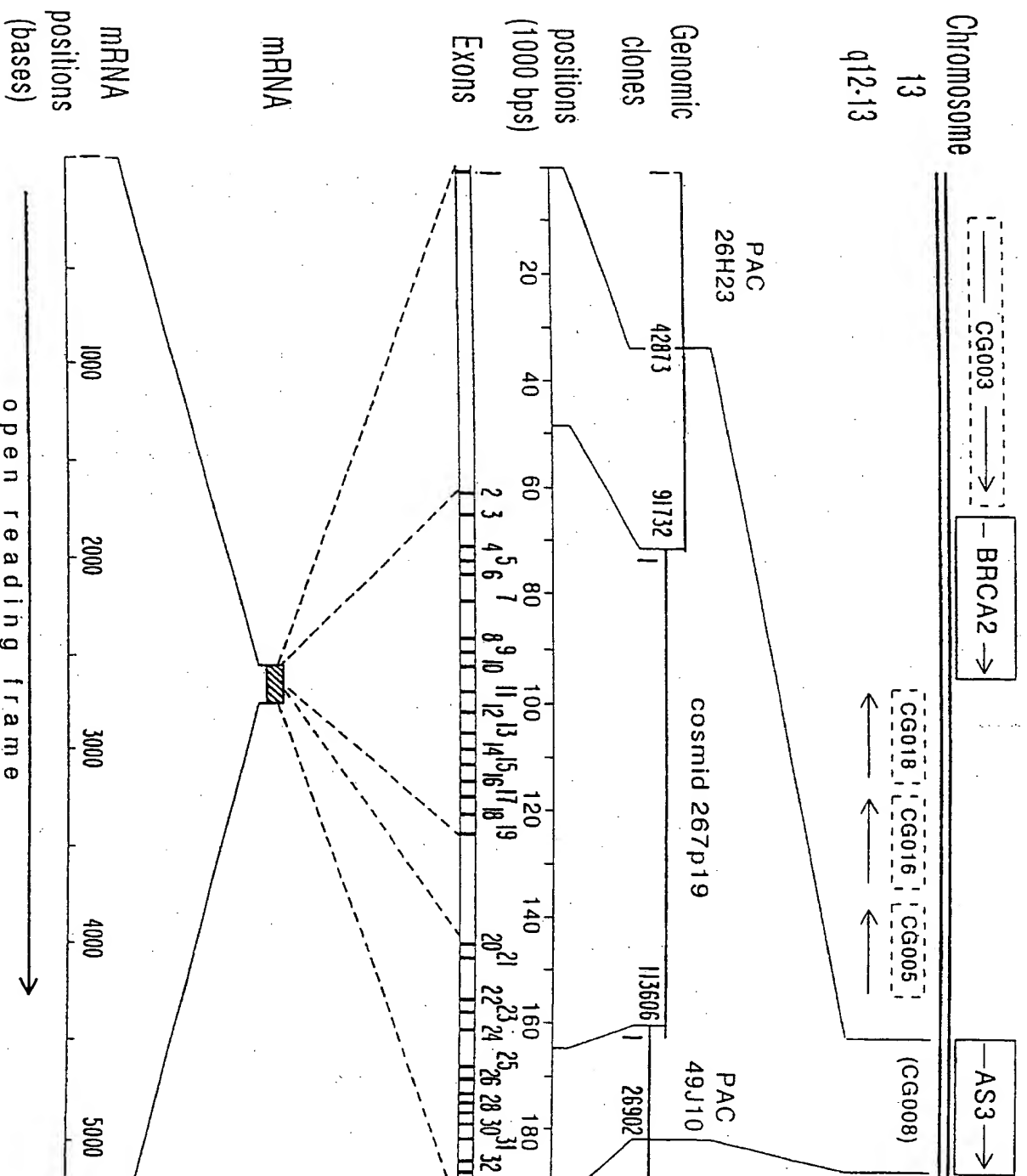
```
{42873}  1                                       46  {42919}
         CCGGAGAG.... Exon 1 ....ACCCGGAG * gtaggaa...


(13347)  47                                      173  (13475)
....ttttcttgtttcag * GGGTAGAA.... Exon 2 ....GATTAAAG * gtgagta...


(16397)  174                                     377  (16602)
..ttttattttgtatag * ATGGTTGT.... Exon 3 ....AACTAAAG * gcaagta...


(22832)  378                                     464  (22920)
..tctttttttatttaag * GATATATT.... Exon 4 ....TACTTGAG * gtaagca...


(23028)  465                                     562  (23125)
.......ccttatttttag * AACATTGC.... Exon 5 ....GTTATAAA * gtaagtt...


(23747)  563                                     689  (23873)
.....ttttgaattgcag * CAATGGCC.... Exon 6 ....CTCATAAG * gtgagta...


(32357)  690                                     854  (32439)
....tttatgttttcag * AATTTAAA.... Exon 7 ....TTACCACT * gtaagtc...


(37809)  855                                     911  (37951)
...ctttctcctcaaaag * TTTTTTAA.... Exon 8 ....AATTAAAG * gtaactt...


(40437)  912                                     1027  (40554)
.......ttttattttag * AGCAATGA.... Exon 9 ....TTGGGCAG * gtatatg...


(43428)  1028                                    1122  (43524)
...tttatattttatcag * GTTTAATG.... Exon 10....CTTAACAG * gtactat...


(48471)  1123                                    1268  (48617)
.....tgttatctttcag * AGTATCTT.... Exon 11....ACAAACGA * gtaagta...


(51727)  1269                                    1420  (51880)
....tttttgttttaag * TGGAGAGT.... Exon 12....GATGATCG * gtaagtt...


(53049)  1421                                    1534  (53164)
...tctgctttttgtag * ACTACTTG.... Exon 13....GCTGTGAA * gtatgtt...
```

FIG. 5-1

```
            (58816)  1535                           1616  (58898)
....tttgtgtttttttcag * AGCATTGA....  Exon 14....AACCCAAA * gtaagta...


            (61447)  1617                           1665  (61497)
...ttgtgtgatttacag * ACAGATGC....  Exon 15....TATTACAA * gtaagtt...


            (64323)  1666                           1805  (64464)
.......tttattttaag * GAAATTTA....  Exon 16....GTTGTGTG * gtaagga...


            (65916)  1806                           1921  (66033)
...taatctgtattacag * CGTGAAAT....  Exon 17....TCTATCAG * gtatttg...


            (71527)  1922                           2027  (71633)
...ttggtcatattttag * TGCTCTTA....  Exon 18....TGCTTAAG * gtaagta...


            (74539)  2028                           2188  (74700)
...tgattcattttatag * GTACTCTC....  Exon 19....ATCAGATC * gtgagtt...


            (96694)  2189                           2312  (96818)
....ttttttttttaatag * AGCCTTGC....  Exon 20....TATTTGAG * gtaatga...


            (99765)  2313                           2471  (99925)
...tcccctcattttcag * CCTCTGCA....  Exon 21....ATGATCGG * gtaattt...


            (105674)  2472                          2540  (105744)
...ctcgtttatttttag * CTTCCAGG....  Exon 22....TGGTCAAA * gtgagta...


            (107185)  2541                          2677  (107322)
...ttgtctcttaaatag * ATTCAGGC....  Exon 23....AAAATTAG * gtatgca...


            (110571)  2678                          2801  (110696)
...ctactcattttttcag * TAAACCAG....  Exon 24....CTATCAAC * gtaagga...


            [4319]  2802                            3006  [4524]
....ttgtgtctttacag * GATGAATG....  Exon 25....TGTTAGTG * gtaagca...
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FIG. 5-2

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      [6829]  3007                          3121  [6945]
.....ttttctttttcag * AAAAATTA.... Exon 26....GTTAAAGA * gtaagac...

      [9074]  3122                          3254  [9208]
.....tttttttttttttag * ATGTCTTT.... Exon 27....TGAATGAA * gtatgta...

      [9522]  3255                          3374  [9642]
.....tatactattgcag * AAACTGTA.... Exon 28....CTGACAAG * gtagtta...

      [10614] 3375                          3437  [10679
...ttctcttggttgtag * AATTTCAG.... Exon 29....CTGGAAAA * gtatgtt...

      [11561] 3438                          3583  [11709]
...catttctcatttcag * CCTAAAAC.... Exon 30....AAGGGGAG * gtaagtg...

      [15476] 3584                          3689  [15583]
...tgtctgtattaaaag * GCTTGATA.... Exon 31....TTGTAAGG * gtgagat...

      21107] 3690                           4129  [21548]
...tttttttttcccctag * TCTGAATT.... Exon 32....CAGCAGAG * gtaagca...

      [21640] 4130                          4354  [21866]
...tcttccccaaagcag * AGCAGAAT.... Exon 33....TACACTAG * gtaagat...

      [26002] 4355                          5253  [26902]
.....ctttccttttaag * GTACGGCG.... Exon 34....GAATGAGT * (poly-A)
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FIG. 5-3